Title: Stress Proteins And Uses Therefor Inventors: Richard A. Young, et al.

FIGURE 1A

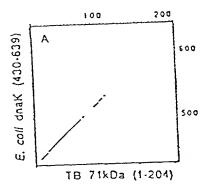
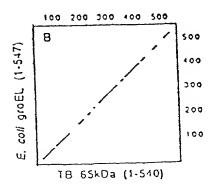


FIGURE 1B



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FIGURE 2

60 50 70 40 30 10 20 MLRLPTVFRQNRPVSRVLAPHLTRAYAKDVKFGADARALNLQGVDLLADAVAVTMGPKGRTVIIEQSWGS UMP1 :::::: :: :: :: :: :: :: :: :: --AKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGA ROEL 120 140 110 90 100 71 80 PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEI **IUMP1** :: : :: PTITKDGVSVAREIEFEDKFENMGAQMVKEVASKANDAAGDGTTTATVLAQAIITEGLKAVAAGMNPMDL BROEL 210 200 180 150 160 170 141 RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE iUMP1 ::::: :: ::: : : :: ::: :::: ::::: : ::: KRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTISANSDETVGKLIAEAMDKVGKEGVITVEDGTGLQDE FROEL 280 270 260 250 230 240 220 211 LEIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG ::: :::::: : :::: : : :: ::: ::::: :::::: LDVVEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEG GROEL ű 350 330 340 310 320 290 300 281 # EALSTLVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV :: : :::::::: :: : : : :: :: :: EALATAVVNTIRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEE-IGMELEKATLEDLGQAKRVVI GROZL 420 410 Part I 390 380 351 360 370 T. TKDDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKD HUMP1 NKDTTTIIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKAF GROEL 49( 460 470 480 450 430 421 VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSL: HUMP1 : ::: ::::::: : ::: :: :: :::: VEDALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEDQNVVSSSL-RAMEAPLRQIVLNCGEEPSV GROEL 540 56 520 550 530 500 510 491 VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMG HUMP1 :: :: ::::: :: :: :: :: :: :: ANTVKGGDGNYGYNAATEEYGNMIDMGILDPTKVTRSALQYAASVAGLMITTECMVTDLPKND-AADLG GROEL 561 570 MGGMGG--GMGGGMF HUMP1 ::::: ::::: AGGMGGMGGMGGMM-GROFT. Total score - 4667, 5 breaks 276 identities out of 545 possible matches between residues 25 random runs Standard deviation -Mean - 3429.48 65.34 SD 18.94 Alignment score =

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Inventors: Richard A. Young, et al. FIGURE 3

	1	10	20	; 30	40	50	60	70	
:UMP1	MLRL	, PTVFRQMRPV	SRVLAPHLTR	LAYAKDVKFG?	.daralmlqgv	DLLADAVAVT	MGPKGRTVII	EQSWGS	
1165K	: M			:: AKTIAYDE	EARRGLERGI	NSLADAVKVI	LGFKGRNVVL	EKKWGA	
	71	80	90	100	110	120	130	140	
:UMP1						TATVLARSIA	KEGFEKISKO	ANPVEI	
:L65K	PTIT	::: :: : NDGVSIAKEI	ETEDAAEKIG	: :: :: GAELVKEVAKI	CTDDVAGDGT	TATVLAQALV		ANPLGL	
	141	150	160	170	180	190	200	210	
:UMP1	RRGV	MLAVDAVIAE	LKKQSKPVTI	PEEIAQVAT	SANGDKEIG	NIISDAMKKVO	RKGVITVKDO	KTLNDE	
:L65k	:: KRGI	::: : EKAVDKVTET	LLKDAKEVET	: :: : : :KEQIAATAA:	::: :: :: :SA-GDQSIGI	: :: ::: DLIAEAMDKVO		NTFGLQ	
	211	220	230	240	250	260	270	280	
:UMP				QKCEFQDAY	JLLSEKKISS:	QSIVPALEIA : ::	NAHRKPLVII • • • • • • • • • • • • • • • • • • •	AEDVDG	
11.65 kg	:: LELT	::: :: ::: EGMRFDKGYI	: :: SGYFVTDAEF	GEYATEELA:	LLVSSKVST	VKDLLPLLEKV	/IQAGKSLLII	AEDVEG	
	281	290	300	310	320	330	340	350	
:UMP	EALS	TLVLNRLKVO				VFGEEGLTLNI			
11.65×	:::: EALS	::: : TLVVNKIRGI	FKSVAVKAPC			: :: :: VISEE-VGLTI			
THE RESERVE OF THE PERSON OF T	351	360	370	380	390	400	410	420	
ERMOE	TKDD.	AMLLKGKGDK	AQIEKRIQE			laklsdgvavi :::: ::::		NEKKDR	
1L65K	TKDE	TTIVEGAGDI	DAIAGRVAQI	RTEIENSDSI	OYDREKLQER:	LAKLAGGVAVI		LKERKHR	
	421	430	440	450	460	470	480	490	
HUMP1	VTDA				LTPANEDQKI	GIEIIKRTLK	PAMTIAKNA(	GVEGSLI	
ML55K	IEDA			:: ::::: LLQAAPALDK:	LKLTGDEAT-	GANIVKVALE		GMEPGV	
	491	500	510	520	530	540	550	56(	
HUMP1	VEKI	MOSSSEVGYE	AMAGDFVNM\	ÆKGIIDPTK	VVRTALLDAA	GVASLLTTAE	VVVTEIPKEE:	KD PGMG,	
ML65K		RNLSVGHGLN	AATGEYEDLI	.KAGVADPVK	VTRSALQNAA.	SIAGLFTT-EA	AVVADKPEKT	AAPASD:	
	561	570							
HUMPI	MGGMGGGMGGGMF								
1L65K		::::::::::::::::::::::::::::::::::::::							
Total 255	score - identit	4552, 7 b ies out of	reaks 540 possi	ble match	es between	residues			
25 ran Alignm	dom run: ent sco:	s ce = 47.	73 SD St	andard de	viation -	23.86	Mean - 341	3.15	

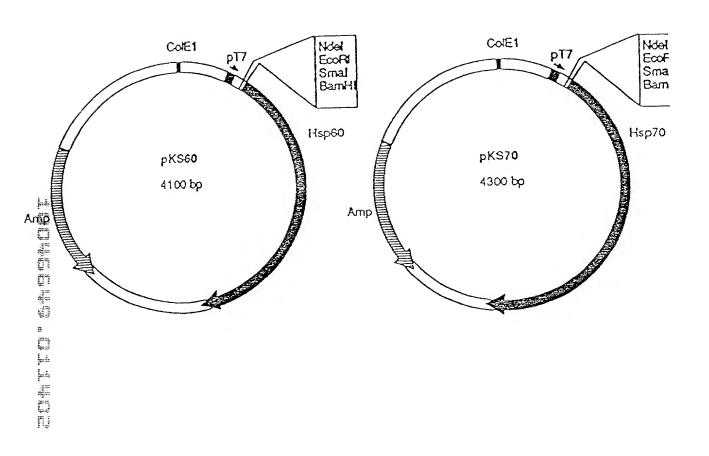
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FIGURE 4

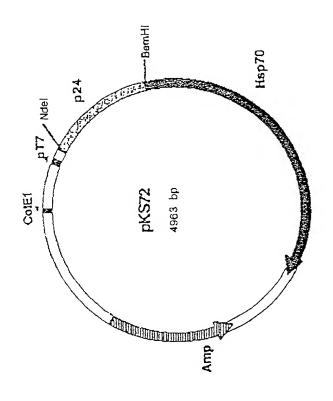
	1	10	20	30	40	50	. 60	7 C				
JUMP1	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIEQSWGS											
:365K	: M			:: AKTIAYDE	:: EARRGLERGL	::::::::::::::::::::::::::::::::::::::		: :: LEKKWG2				
	71	80	90	100	110	120	130	140				
:UMP1	, PKVI	' 'KDGVTVAKS	DLKDKYKNIC	, AKLVODVANA	, Theeagdgtt	' TATVLARSIA	, AKEGFEKISKO	, GANPVET				
:365K	: :	::: :: :	::::::	: :: ::		::::::	:::	::::				
				. = .								
	141	150	160	170	180	190	200	21(				
IB6 3k	::	:: :	:::::	: :: : :	(SANGDKEIGN  -:::  SA-GDQSIGD	: :: :::	:::::	:				
### 101   102   103   10	211	220	230	240	250	260	270	28(				
HUMBI		EGMKFDRGYI	SPYFINTSKO	-	LLSEKKISSI	-	NAHRKPLVII	AEDVDC				
736 <b>5</b> 7	:: LELT	EGMRFDKGYI	SGYFVTDPER	: : QEAVLEDPYI	LLVSSKVSTV	KDLLPLLEKV	'IGAGKPLLI	AEDVE				
# #***********************************	281	290	300	310	320	330	340	35				
HUKPA Pa T36 gg:	::::	::::	::::::	::: :: :	DMAIATGGAV :::::::::::::::::::::::::::::::::::	:: ::	: :::	:				
	351	360	370	380	390	400	410	42				
HUMPl	TKDD	AMLLKGKGDK	-		YEKEKLNERL			NEKKD				
T365K	TKDE	TTIVEGAGDT	: : : DAIAGRVAQI		: ::: ::: YDREKLQERL			KERKH				
	421	430	440	450	460	470	480	49				
HUMP1		LNATRAAVEE			TPANEDQKIG	IEIIKRTLKI	PAMTIAKNAC	SVEGSI				
T365K	:: IEDA	:::: EEVAAAVEE		: :::: LQAAPTLDEL	: : K-LEGDEATG	: : : ANIVKVALEA	: :::: .PLKQIAFNSC	: : :LEPG\				
	491	500	510	520	530	540	550	5,				
HUMP1	VEKI	MQSSSEVGYD.	AMAGDEVNMV	EKGIIDPTKV	VRTALLDAAG	, VASLLTTAEV	, VVTE1PKESH	CDPGM(				
Т365К	AEKVE		: : AQTGVYEDLL	: :: :: AAGVADPVKV	: :: :: TRSALQNAAS	: : : : IAGLFLTTEA	:: :: VVADKPEKER	(ASVP)				
	561											
HUMP1		, GGMGGGMF										
TB65K	:: ::: : GGDMGGMDF											
Total : 257	score - identiti	4560, 5 bi	reaks 540 possil	ole matche	s between :	residues						
25 rand Alignme	dem runs ent scor	e = 49.3	36 SD Sta	andard dev	iation =	23.23 M	ean - 3413	.15				

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Figure 5



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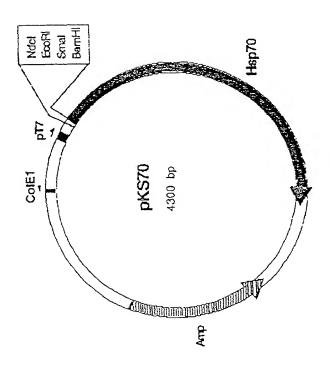
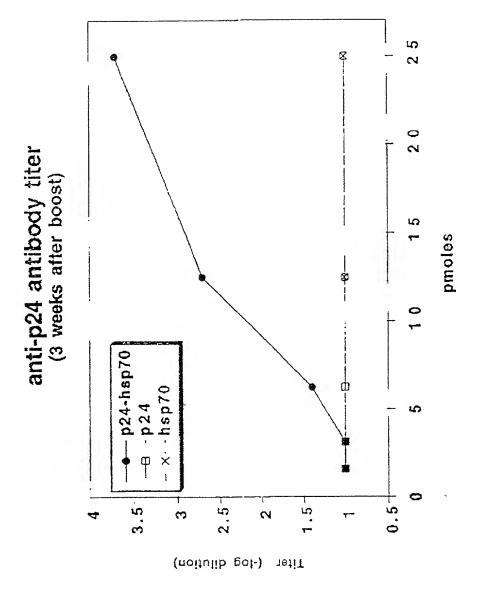


FIGURE 6

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FIGHRE 7